

09/762045

WO 00/08169

PCT/EP99/05467

SEQUENZPROTOKOLL

JC07 Rec'd PCT/PTO 01 FEB 2001

<110> SunGene GmbH & Co. KGaA

<120> DNA-Sequenz kodierend fuer eine  
1-Deoxy-D-xylulose-5-phosphat Synthase

<130> 0050/49249

<140> 0817 - 00006

<141> 1999-08-04

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<170> PatentIn Vers. 2.0

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Gly Leu Ser Thr Asp Ser Cys Lys Ser Thr Ser Leu Ser Ser Ser Arg  
20 25 30

tct ttg gtt aca gat ctt cca tca cca tgt ctg aaa ccc aac aac aat 144  
Ser Leu Val Thr Asp Leu Pro Ser Pro Cys Leu Lys Pro Asn Asn Asn  
35 40 45

tcc cat tca aac aga aga gca aaa gtg tgt gct tca ctt gca gag aag 192  
Ser His Ser Asn Arg Arg Ala Lys Val Cys Ala Ser Leu Ala Glu Lys  
50 55 60

ggg gaa tat tat tca aac aga cca cca act cca tta ctt gac act att 240  
Gly Glu Tyr Tyr Ser Asn Arg Pro Pro Thr Pro Leu Leu Asp Thr Ile  
65 70 75 80

aac tac cca atc cac atg aaa aat ctt tct gtc aag gaa ctg aaa caa 288  
Asn Tyr Pro Ile His Met Lys Asn Leu Ser Val Lys Glu Leu Lys Gln

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90

95

ctt tct gat gag ctg aga tca gac gtg atc ttt aat gtg tcg aaa acc 336  
 Leu Ser Asp Glu Leu Arg Ser Asp Val Ile Phe Asn Val Ser Lys Thr  
 100 105 110

ggt gga cat ttg ggg tca agt ctt ggt gtt gtg gag ctt act gtg gct 384  
 Gly Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala  
 115 120 125

ctt cat tac att ttc aat act cca caa gac aag att ctt tgg gat gtt 432  
 Leu His Tyr Ile Phe Asn Thr Pro Gln Asp Lys Ile Leu Trp Asp Val  
 130 135 140

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 Gly His Gln Ser Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Gly Lys  
 145 150 155 160

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 Ile Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Lys Gly Lys  
 195 200 205

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 Gln Ala Tyr Glu Ala Met Asn Asn Ala Gly Tyr Leu Asp Ser Asp Met  
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att gtg att ctt aat gac aac aag caa gtc tca tta cct aca gct act 768  
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 260 265 270

cgg tta cag tct aac ccg gct ctc aga gag ttg aga gaa gtc gca aag 864  
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280

285

ggt atg aca aag caa ata ggc gga cca atg cat cag ttg gcg gct aag 912  
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gta gat gtg tat gct cga gga atg ata agc ggt act gga tcg tca ctg 960  
 Val Asp Val Tyr Ala Arg Gly Met Ile Ser Gly Thr Gly Ser Ser Leu  
 305 310 315 320

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 Phe Glu Glu Leu Gly Leu Tyr Tyr Ile Gly Pro Val Asp Gly His Asn  
 325 330 335

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aca gga cct gta ctt att cat gtg gtg acg gag aaa ggt cgt ggt tat 1104  
 Thr Gly Pro Val Leu Ile His Val Val Thr Glu Lys Gly Arg Gly Tyr  
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cct tac gcg gag aga gct gat gac aaa tac cat ggt gtt gtg aaa ttt 1152  
 Pro Tyr Ala Glu Arg Ala Asp Asp Lys Tyr His Gly Val Val Lys Phe  
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 Asp Pro Ala Thr Gly Arg Gln Phe Lys Thr Thr Asn Glu Thr Gln Ser  
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tac aca act tac ttt gcg gag gca tta gtc gca gaa gca gag gta gac 1248  
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 Lys Asp Val Val Ala Ile His Ala Ala Met Gly Gly Thr Gly Leu  
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aat ctc ttt caa cgt cgc ttc cca aca aga tgt ttc gat gta gga ata 1344  
 Asn Leu Phe Gln Arg Arg Phe Pro Thr Arg Cys Phe Asp Val Gly Ile  
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gcg gaa caa cac gca gtt act ttt gct gcg ggt tta gcc tgt gaa ggc 1392  
 Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Cys Glu Gly  
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485	490	495		
gca atg gat aga gct gga ctc gtt gga gct gat ggt ccg aca cat tgt Ala Met Asp Arg Ala Gly Leu Val Gly Ala Asp Gly Pro Thr His Cys				1536
500	505	510		
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515	520	525		
atg gct cca tca gat gaa gca gat ctc ttt aac atg gtt gca act gct Met Ala Pro Ser Asp Glu Ala Asp Leu Phe Asn Met Val Ala Thr Ala				1632
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565	570	575		
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580	585	590		
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610	615	620		
cca ttg gac cgt gct ctc att cgc agc tta gct aag tcg cac gag gtt Pro Leu Asp Arg Ala Leu Ile Arg Ser Leu Ala Lys Ser His Glu Val				1920
625	630	635	640	
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645	650	655		
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660

665

670

aga cca atg gta ctg cct gat cga tac att gat cac ggt gca cca gct 2064  
Arg Pro Met Val Leu Pro Asp Arg Tyr Ile Asp His Gly Ala Pro Ala  
675 680 685

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Asp Gln Leu Ala Glu Ala Gly Leu Met Pro Ser His Ile Ala Ala Thr  
690 695 700

gca ctt aac tta atc ggt gca cca agg gaa gct ctg ttt tga 2154  
Ala Leu Asn Leu Ile Gly Ala Pro Arg Glu Ala Leu Phe  
705 710 715

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35 40 45

Ser His Ser Asn Arg Arg Ala Lys Val Cys Ala Ser Leu Ala Glu Lys  
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Gly Glu Tyr Tyr Ser Asn Arg Pro Pro Thr Pro Leu Leu Asp Thr Ile  
65 70 75 80

Asn Tyr Pro Ile His Met Lys Asn Leu Ser Val Lys Glu Leu Lys Gln  
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Leu Ser Asp Glu Leu Arg Ser Asp Val Ile Phe Asn Val Ser Lys Thr  
100 105 110

Gly Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala  
115 120 125

Leu His Tyr Ile Phe Asn Thr Pro Gln Asp Lys Ile Leu Trp Asp Val  
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Gly His Gln Ser Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Gly Lys  
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Met Pro Thr Met Arg Gln Thr Asn Gly Leu Ser Gly Phe Thr Lys Arg  
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Gly Glu Ser Glu His Asp Cys Phe Gly Thr Gly His Ser Ser Thr Thr  
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Ile Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Lys Gly Lys  
195 200 205

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210 215 220

Gln Ala Tyr Glu Ala Met Asn Asn Ala Gly Tyr Leu Asp Ser Asp Met  
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Ile Val Ile Leu Asn Asp Asn Lys Gln Val Ser Leu Pro Thr Ala Thr  
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Leu Asp Gly Pro Ser Pro Pro Val Gly Ala Leu Ser Ser Ala Leu Ser  
260 265 270

Arg Leu Gln Ser Asn Pro Ala Leu Arg Glu Leu Arg Glu Val Ala Lys  
275 280 285

Gly Met Thr Lys Gln Ile Gly Gly Pro Met His Gln Leu Ala Ala Lys  
290 295 300

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305 310 315 320

Phe Glu Glu Leu Gly Leu Tyr Tyr Ile Gly Pro Val Asp Gly His Asn  
325 330 335

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340 345 350

Thr Gly Pro Val Leu Ile His Val Val Thr Glu Lys Gly Arg Gly Tyr  
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Pro Tyr Ala Glu Arg Ala Asp Asp Lys Tyr His Gly Val Val Lys Phe  
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Asp Pro Ala Thr Gly Arg Gln Phe Lys Thr Thr Asn Glu Thr Gln Ser  
385 390 395 400

Tyr Thr Thr Tyr Phe Ala Glu Ala Leu Val Ala Glu Ala Glu Val Asp  
405 410 415

Lys Asp Val Val Ala Ile His Ala Ala Met Gly Gly Thr Gly Leu  
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Asn Leu Phe Gln Arg Arg Phe Pro Thr Arg Cys Phe Asp Val Gly Ile  
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Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Cys Glu Gly  
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Asp Gln Val Val His Asp Val Asp Leu Gln Lys Leu Pro Val Arg Phe  
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Gly Ala Phe Asp Val Thr Phe Met Ala Cys Leu Pro Asn Met Ile Val  
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Gly Ile Gly Val Ala Leu Pro Pro Gly Asn Lys Gly Val Pro Ile Glu  
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Ile Gly Lys Gly Arg Ile Leu Lys Glu Gly Glu Arg Val Ala Leu Leu  
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610 615 620

Pro Leu Asp Arg Ala Leu Ile Arg Ser Leu Ala Lys Ser His Glu Val  
625 630 635 640

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Val Gln Phe Leu Ala Leu Asp Gly Leu Leu Asp Gly Lys Leu Lys Trp  
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Tyr	Val	Tyr	Asn	Thr	Pro	Phe	Asp	Gln	Leu	Ile	Trp	Asp	Val	Gly	His	
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cag gct tat ccg cat aaa att ttg acc gga cgc cgc gac aaa atc ggc															288	
Gln	Ala	Tyr	Pro	His	Lys	Ile	Leu	Thr	Gly	Arg	Arg	Asp	Lys	Ile	Gly	
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acc atc cgt cag aaa ggc ggt ctg cac ccg ttc ccg tgg cgc ggc gaa															336	
Thr	Ile	Arg	Gln	Lys	Gly	Gly	Leu	His	Pro	Phe	Pro	Trp	Arg	Gly	Glu	
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Ser	Glu	Tyr	Asp	Val	Leu	Ser	Val	Gly	His	Ser	Ser	Thr	Ser	Ile	Ser	
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gcc gga att ggt att gcg gtt gct gcc gaa aaa gaa ggc aaa aat cgc															432	
Ala	Gly	Ile	Gly	Ile	Ala	Val	Ala	Ala	Glu	Lys	Glu	Gly	Lys	Asn	Arg	
130				135					140							
cgc acc gtc tgt gtc att ggc gat ggc gcg att acc gca ggc atg gcg															480	
Arg	Thr	Val	Cys	Val	Ile	Gly	Asp	Gly	Ala	Ile	Thr	Ala	Gly	Met	Ala	
145				150					155			160				
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Phe	Glu	Ala	Met	Asn	His	Ala	Gly	Asp	Ile	Arg	Pro	Asp	Met	Leu	Val	
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att ctc aac gac aat gaa atg tcg att tcc gaa aat gtc ggc gcg ctc															576	
Ile	Leu	Asn	Asp	Asn	Glu	Met	Ser	Ile	Ser	Glu	Asn	Val	Gly	Ala	Leu	
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cgc gaa ggc ggg aaa aaa gtt ttc tct ggc gtg ccg cca att aaa gag															672	
Arg	Glu	Gly	Gly	Lys	Val	Phe	Ser	Gly	Val	Pro	Pro	Ile	Lys	Glu		
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ctg ctc aaa cgc acc gaa gaa cat att aaa ggc atg gta gtg cct ggc															720	
Leu	Leu	Lys	Arg	Thr	Glu	Glu	His	Ile	Lys	Gly	Met	Val	Val	Pro	Gly	
225					230				235			240				
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Thr Leu Phe Glu Glu Leu Gly Phe Asn Tyr Ile Gly Pro Val Asp Gly  
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cac gat gtg ctg ggg ctt atc acc acg cta aag aac atg cgc gac ctg 816  
 His Asp Val Leu Gly Leu Ile Thr Thr Leu Lys Asn Met Arg Asp Leu  
 260 265 270

aaa ggc ccg cag ttc ctg cat atc atg acc aaa aaa ggt cgt ggt tat 864  
 Lys Gly Pro Gln Phe Leu His Ile Met Thr Lys Lys Gly Arg Gly Tyr  
 275 280 285

gaa ccg gca gaa aaa gac ccg atc act ttc cac gcc gtg cct aaa ttt 912  
 Glu Pro Ala Glu Lys Asp Pro Ile Thr Phe His Ala Val Pro Lys Phe  
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gat ccc tcc agc ggt tgt ttg ccg aaa agt agc ggc ggt ttg ccg agc 960  
 Asp Pro Ser Ser Gly Cys Leu Pro Lys Ser Ser Gly Gly Leu Pro Ser  
 305 310 315 320

tat tca aaa atc ttt ggc gac tgg ttg tgc gaa acg gca gcg aaa gac 1008  
 Tyr Ser Lys Ile Phe Gly Asp Trp Leu Cys Glu Thr Ala Ala Lys Asp  
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 Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Ile Gly Gly  
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tac aaa ccc att gtc gcg att tac tcc act ttc ctgcaa cgc gcc tat 1200  
 Tyr Lys Pro Ile Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr  
 385 390 395 400

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Gly Ala Phe Asp Leu Ser Tyr Leu Arg Cys Ile Pro Glu Met Val Ile  
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 Ala Val Gly Val Glu Leu Thr Pro Leu Glu Lys Leu Pro Ile Gly Lys  
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gaa atg gcc gcc agc cat gaa gcg ctg gtc acc gta gaa gaa aac gcc 1680  
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 545 550 555 560

att atg ggc ggc gca ggc agc ggc gtg aac gaa gtg ctg atg gcc cat 1728  
 Ile Met Gly Gly Ala Gly Ser Gly Val Asn Glu Val Leu Met Ala His  
 565 570 575

cgt aaa cca gta ccc gtg ctg aac att ggc ctg ccg gac ttc ttt att 1776  
 Arg Lys Pro Val Pro Val Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile  
 580 585 590

ccg caa gga act cag gaa gaa atg cgc gcc gaa ctc ggc ctc gat gcc 1824  
 Pro Gln Gly Thr Gln Glu Glu Met Arg Ala Glu Leu Gly Leu Asp Ala  
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gct ggt atg gaa gcc aaa atc aag gcc tgg ctg gca taa 1863  
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&lt;211&gt; 620

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Asp Glu Leu Arg Arg Tyr Leu Leu Asp Ser Val Ser Arg Ser Ser Gly  
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Tyr Val Tyr Asn Thr Pro Phe Asp Gln Leu Ile Trp Asp Val Gly His  
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Gln Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Ile Gly  
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Thr Ile Arg Gln Lys Gly Leu His Pro Phe Pro Trp Arg Gly Glu  
100 105 110

Ser Glu Tyr Asp Val Leu Ser Val Gly His Ser Ser Thr Ser Ile Ser  
115 120 125

Ala Gly Ile Gly Ile Ala Val Ala Ala Glu Lys Glu Gly Lys Asn Arg  
130 135 140

Arg Thr Val Cys Val Ile Gly Asp Gly Ala Ile Thr Ala Gly Met Ala  
145 150 155 160

Phe Glu Ala Met Asn His Ala Gly Asp Ile Arg Pro Asp Met Leu Val  
165 170 175

Ile Leu Asn Asp Asn Glu Met Ser Ile Ser Glu Asn Val Gly Ala Leu  
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Asn Asn His Leu Ala Gln Leu Leu Ser Gly Lys Leu Tyr Ser Ser Leu  
195 200 205

Arg Glu Gly Gly Lys Lys Val Phe Ser Gly Val Pro Pro Ile Lys Glu  
210 215 220

Leu Leu Lys Arg Thr Glu Glu His Ile Lys Gly Met Val Val Pro Gly  
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260 265 270

Lys Gly Pro Gln Phe Leu His Ile Met Thr Lys Lys Gly Arg Gly Tyr  
275 280 285

Glu Pro Ala Glu Lys Asp Pro Ile Thr Phe His Ala Val Pro Lys Phe  
290 295 300

Asp Pro Ser Ser Gly Cys Leu Pro Lys Ser Ser Gly Gly Leu Pro Ser  
305 310 315 320

Tyr Ser Lys Ile Phe Gly Asp Trp Leu Cys Glu Thr Ala Ala Lys Asp  
325 330 335

Asn Lys Leu Met Ala Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Met  
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Val Glu Phe Ser Arg Lys Phe Pro Asp Arg Tyr Phe Asp Val Ala Ile  
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Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Ile Gly Gly  
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Tyr Lys Pro Ile Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr  
385 390 395 400

Asp Gln Val Leu His Asp Val Ala Ile Gln Lys Leu Pro Val Leu Phe  
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Ala Ile Asp Arg Ala Gly Ile Val Gly Ala Asp Gly Gln Thr His Gln  
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Gly Ala Phe Asp Leu Ser Tyr Leu Arg Cys Ile Pro Glu Met Val Ile  
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Met Thr Pro Ser Asp Glu Asn Glu Cys Arg Gln Met Leu Tyr Thr Gly  
450 455 460

Tyr His Tyr Asn Asp Gly Pro Ser Ala Val Arg Tyr Pro Arg Gly Asn  
465 470 475 480

Ala Val Gly Val Glu Leu Thr Pro Leu Glu Lys Leu Pro Ile Gly Lys  
485 490 495

Gly Ile Val Lys Arg Arg Gly Glu Lys Leu Ala Ile Leu Asn Phe Gly  
500 505 510

Thr Leu Met Pro Glu Ala Ala Lys Val Ala Glu Ser Leu Asn Ala Thr  
515 520 525

Leu Val Asp Met Arg Phe Val Lys Pro Leu Asp Glu Ala Leu Ile Leu  
530 535 540

Glu Met Ala Ala Ser His Glu Ala Leu Val Thr Val Glu Glu Asn Ala  
545 550 555 560

Ile Met Gly Gly Ala Gly Ser Gly Val Asn Glu Val Leu Met Ala His  
565 570 575

Arg Lys Pro Val Pro Val Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile  
580 585 590

Pro Gln Gly Thr Gln Glu Glu Met Arg Ala Glu Leu Gly Leu Asp Ala  
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Ala Gly Met Glu Ala Lys Ile Lys Ala Trp Leu Ala  
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<212> DNA

<213> Streptomyces avermitilis

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<221> CDS

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gagcaactccg atgcgcggct cccgcgcctc cagcaccagg agccggccgt ccagatgatc 180

gatcgccacg gcagccccctc cagtggtcat cctgtac atg cag ccc cac gcc atg 235  
Met Gln Pro His Ala Met

ggc ggt gca ctg aac aca ttg tcc agc gga caa gcc aac tat tgc gca 283  
 Gly Gly Ala Leu Asn Thr Leu Ser Ser Gly Gln Ala Asn Tyr Cys Ala  
     10                 15                 20

cct tgc gga acg gag cga ccc tgc cgc cat gac gca gac cac aca cca 331  
 Pro Cys Gly Thr Glu Arg Pro Cys Arg His Asp Ala Asp His Thr Pro  
     25                 30                 35

cac tcc cga cac cgc ccg gca ggc cga ccc ctt ccc ggt gaa ggg aat 379  
 His Ser Arg His Arg Pro Ala Gly Arg Pro Leu Pro Gly Glu Gly Asn  
     40                 45                 50

gga cgc ggt cgt ctt cgc cgt agg caa cgc caa gca ggc cgc gca cta 427  
 Gly Arg Gly Arg Leu Arg Arg Gln Arg Gln Ala Gly Arg Ala Leu  
     55                 60                 65                 70

ctc cac cgc ctt cgg cat gca gct tgt ggc gta ctc cgg acc gga gaa 475  
 Leu His Arg Leu Arg His Ala Ala Cys Gly Val Leu Arg Thr Gly Glu  
     75                 80                 85

cgg cag ccg cga gac cgc ttc gta cgt cct cac caa cgg ctc ggc acg 523  
 Arg Gln Pro Arg Asp Arg Phe Val Arg Pro His Gln Arg Leu Gly Thr  
     90                 95                 100

ctt cgt cct cac ctc cgt cat caa gcc cgc cac ccc ctg ggg cca ctt 571  
 Leu Arg Pro His Leu Arg His Gln Ala Arg His Pro Leu Gly Pro Leu  
     105                110                115

cct cgc cga cca tgt ggc cga gca cgg cga cgg cgt cgt cga cct cgc 619  
 Pro Arg Arg Pro Cys Gly Arg Ala Arg Arg Arg Arg Arg Pro Arg  
     120                125                130

cat cga ggt ccc gga cgc ccg cgc cgc cca cgc gta cgc gat cga gca 667  
 His Arg Gly Pro Gly Arg Pro Arg Arg Pro Arg Val Arg Asp Arg Ala  
     135                140                145                150

cgg cgc ccg ctc ggt cgc cga gcc gta cga gct gaa gga cga gca cgg 715  
 Arg Arg Pro Leu Gly Arg Arg Ala Val Arg Ala Glu Gly Arg Ala Arg  
     155                160                165

cac ggt cgt cct cgc cgc gat cgc cac cta cgg caa gac ccg cca cac 763  
 His Gly Arg Pro Arg Arg Asp Arg His Leu Arg Gln Asp Pro Pro His  
     170                175                180

cct cgt cga ccg gac cgg cta cga cgg ccc cta cct ccc cgg cta cgt 811  
 Pro Arg Arg Pro Asp Arg Leu Arg Arg Pro Leu Pro Pro Arg Leu Arg  
     185                190                195

ggc cgc cgc ccc gat cgt cga acc gcc cgc cca ccg cac ctt cca ggc 859  
 Gly Arg Arg Pro Asp Arg Arg Thr Ala Arg Pro Pro His Leu Pro Gly  
 200 205 210

cat cga cca ctg cgt cggt caa cgt cga gct cggt ccg gat gaa cga atg 907  
 His Arg Pro Leu Arg Arg Gln Arg Arg Ala Arg Pro Asp Glu Arg Met  
 215 220 225 230

ggt cgg ctt cta caa caa ggt cat ggg ctt cac gaa cat gaa gga gtt 955  
 Gly Arg Leu Leu Gln Gln Gly His Gly Leu His Glu His Glu Gly Val  
 235 240 245

cgt ggg cga cga cat cgc gac cga gta ctc ggc gct gat gtc gaa ggt 1003  
 Arg Gly Arg Arg His Arg Asp Arg Val Leu Gly Ala Asp Val Glu Gly  
 250 255 260

cgt ggc cga cgg cac gct caa ggt caa gtt ccc gat caa cga gcc cgc 1051  
 Arg Gly Arg Arg His Ala Gln Gln Val Pro Asp Gln Arg Ala Arg  
 265 270 275

cct cgc caa gaa gaa gtc cca gat cga cga gta cct gga gtt cta cgg 1099  
 Pro Arg Gln Glu Glu Val Pro Asp Arg Arg Val Pro Gly Val Leu Arg  
 280 285 290

cgg cgc ggg cgt cca gca cat cgc gct gaa cac ggg tga catcgatcgag 1148  
 Arg Arg Gly Arg Pro Ala His Arg Ala Glu His Gly  
 295 300 305

acggtagcga cgatgcgcgc cgccggcgtc cagttcctgg acacgcccga ctcgtactac 1208

gacaccctcg gggagtgggt gggcgacacc cgcgcccccg tcgacaccct gcgcgagctg 1268

aagatcctcg cggaccgcga cgaggacggc tatctgctcc agatcttac caagccggtc 1328

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&lt;211&gt; 306

&lt;212&gt; PRT

&lt;213&gt; Streptomyces avermitilis

&lt;400&gt; 6

Met Gln Pro His Ala Met Gly Gly Ala Leu Asn Thr Leu Ser Ser Gly

1

5

10

15

Gln Ala Asn Tyr Cys Ala Pro Cys Gly Thr Glu Arg Pro Cys Arg His  
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Asp Ala Asp His Thr Pro His Ser Arg His Arg Pro Ala Gly Arg Pro  
35 40 45

Leu Pro Gly Glu Gly Asn Gly Arg Gly Arg Leu Arg Arg Arg Gln Arg  
50 55 60

Gln Ala Gly Arg Ala Leu Leu His Arg Leu Arg His Ala Ala Cys Gly  
65 70 75 80

Val Leu Arg Thr Gly Glu Arg Gln Pro Arg Asp Arg Phe Val Arg Pro  
85 90 95

His Gln Arg Leu Gly Thr Leu Arg Pro His Leu Arg His Gln Ala Arg  
100 105 110

His Pro Leu Gly Pro Leu Pro Arg Arg Pro Cys Gly Arg Ala Arg Arg  
115 120 125

Arg Arg Arg Arg Pro Arg His Arg Gly Pro Gly Arg Pro Arg Arg Pro  
130 135 140

Arg Val Arg Asp Arg Ala Arg Arg Pro Leu Gly Arg Arg Ala Val Arg  
145 150 155 160

Ala Glu Gly Arg Ala Arg His Gly Arg Pro Arg Arg Asp Arg His Leu  
165 170 175

Arg Gln Asp Pro Pro His Pro Arg Arg Pro Asp Arg Leu Arg Arg Pro  
180 185 190

Leu Pro Pro Arg Leu Arg Gly Arg Arg Pro Asp Arg Arg Thr Ala Arg  
195 200 205

Pro Pro His Leu Pro Gly His Arg Pro Leu Arg Arg Gln Arg Arg Ala  
210 215 220

Arg Pro Asp Glu Arg Met Gly Arg Leu Leu Gln Gln Gly His Gly Leu  
225 230 235 240

His Glu His Glu Gly Val Arg Gly Arg Arg His Arg Asp Arg Val Leu  
245 250 255

Gly Ala Asp Val Glu Gly Arg Gly Arg Arg His Ala Gln Gly Gln Val

260

265

270

Pro Asp Gln Arg Ala Arg Pro Arg Gln Glu Glu Val Pro Asp Arg Arg  
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Val Pro Gly Val Leu Arg Arg Arg Gly Arg Pro Ala His Arg Ala Glu  
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His Gly  
305

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&lt;211&gt; 1479

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

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&lt;222&gt; (1)..(1401)

&lt;400&gt; 7

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tca acg gag caa aca aac ttc gtc tct cat gta ccg tca tca ctt tct 96  
Ser Thr Glu Gln Thr Asn Phe Val Ser His Val Pro Ser Ser Leu Ser  
20 25 30

ctc cct caa cga cgg acc tct ctc cga gta acc gca gcc agg gcc act 144  
Leu Pro Gln Arg Arg Thr Ser Leu Arg Val Thr Ala Ala Arg Ala Thr  
35 40 45

ccc aaa ctc tcc aac cgt aaa ctc cgt gtc gcc gtc atc ggt ggt gga 192  
Pro Lys Leu Ser Asn Arg Lys Leu Arg Val Ala Val Ile Gly Gly Gly  
50 55 60

cca gca ggc ggg gca gct gca gag act cta gca caa gga gga atc gag 240  
Pro Ala Gly Gly Ala Ala Ala Glu Thr Leu Ala Gln Gly Gly Ile Glu  
65 70 75 80

acg att ctc atc gag cgt aag atg gac aat tgc aag cct tgc ggt ggc 288  
Thr Ile Leu Ile Glu Arg Lys Met Asp Asn Cys Lys Pro Cys Gly Gly  
85 90 95

gcg att cct ctc tgt atg gtc gga gaa ttc aac ttg ccg ttg gat att 336  
Ala Ile Pro Leu Cys Met Val Gly Glu Phe Asn Leu Pro Leu Asp Ile

100

105

110

att gat cgg aga gtg acg aag atg aag atg att tcg ccg tcg aac att 384  
 Ile Asp Arg Arg Val Thr Lys Met Lys Met Ile Ser Pro Ser Asn Ile  
 115 120 125

gct gtt gat att ggt cgt acg ctt aag gag cat gag tat ata ggt atg 432  
 Ala Val Asp Ile Gly Arg Thr Leu Lys Glu His Glu Tyr Ile Gly Met  
 130 135 140

gtg aga aga gaa gtt ctt gat gct tat ctg aga gag aga gct gag aag 480  
 Val Arg Arg Glu Val Leu Asp Ala Tyr Leu Arg Glu Arg Ala Glu Lys  
 145 150 155 160

agt gga gcc act gtg att aac ggt ctc ttc ctt aag atg gat cat ccg 528  
 Ser Gly Ala Thr Val Ile Asn Gly Leu Phe Leu Lys Met Asp His Pro  
 165 170 175

gag aat tgg gac tcg ccg tac act ttg cat tac act gag tac gat ggt 576  
 Glu Asn Trp Asp Ser Pro Tyr Thr Leu His Tyr Thr Glu Tyr Asp Gly  
 180 185 190

aaa act gga gct aca ggg acg aag aaa aca atg gag gtt gat gct gtc 624  
 Lys Thr Gly Ala Thr Gly Thr Lys Lys Thr Met Glu Val Asp Ala Val  
 195 200 205

att gga gct gat gga gct aac tct agg gtt gct aaa tct att gat gct 672  
 Ile Gly Ala Asp Gly Ala Asn Ser Arg Val Ala Lys Ser Ile Asp Ala  
 210 215 220

ggt gat tac gac tac gca att gca ttt cag gag agg att agg att cct 720  
 Gly Asp Tyr Asp Tyr Ala Ile Ala Phe Gln Glu Arg Ile Arg Ile Pro  
 225 230 235 240

gat gag aaa atg act tac tat gag gat tta gct gag atg tat gtt gga 768  
 Asp Glu Lys Met Thr Tyr Tyr Glu Asp Leu Ala Glu Met Tyr Val Gly  
 245 250 255

gat gat gtg tcg ccg gat ttc tat ggt tgg gtg ttc cct aag tgc gac 816  
 Asp Asp Val Ser Pro Asp Phe Tyr Gly Trp Val Phe Pro Lys Cys Asp  
 260 265 270

cat gta gct gtt gga aca ggt act gtg act cac aaa ggt gac atc aag 864  
 His Val Ala Val Gly Thr Gly Thr Val Thr His Lys Gly Asp Ile Lys  
 275 280 285

aag ttc cag ctc gcg acc aga aac aga gct aag gac aag att ctt gga 912  
 Lys Phe Gln Leu Ala Thr Arg Asn Arg Ala Lys Asp Lys Ile Leu Gly

290	295	300	
ggg aag atc atc cgt gtg gag gct cat ccg att cct gaa cat ccg aga 960 Gly Lys Ile Ile Arg Val Glu Ala His Pro Ile Pro Glu His Pro Arg			
305	310	315	320
cca cgt agg ctc tcg aaa cgt gtg gct ctt gta ggt gat gct gca ggg 1008 Pro Arg Arg Leu Ser Lys Arg Val Ala Leu Val Gly Asp Ala Ala Gly			
325	330	335	
tat gtg act aaa tgc tct ggt gaa ggg atc tac ttt gct gct aag agt 1056 Tyr Val Thr Lys Cys Ser Gly Glu Gly Ile Tyr Phe Ala Ala Lys Ser			
340	345	350	
gga aga atg tgt gct gaa gcc att gtc gaa ggt tca cag aat ggt aag 1104 Gly Arg Met Cys Ala Glu Ala Ile Val Glu Gly Ser Gln Asn Gly Lys			
355	360	365	
aag atg att gac gaa ggg gac ttg agg aag tac ttg gag aaa tgg gat 1152 Lys Met Ile Asp Glu Gly Asp Leu Arg Lys Tyr Leu Glu Lys Trp Asp			
370	375	380	
aag aca tac ttg cct acc tac agg gta ctt gat gtg ttg cag aaa gtg 1200 Lys Thr Tyr Leu Pro Thr Tyr Arg Val Leu Asp Val Leu Gln Lys Val			
385	390	395	400
ttt tac aga tca aat ccg gct aga gaa gcg ttt gtg gag atg tgt aat 1248 Phe Tyr Arg Ser Asn Pro Ala Arg Glu Ala Phe Val Glu Met Cys Asn			
405	410	415	
gat gag tat gtt cag aag atg aca ttc gat agc tat ctg tac aag cgg 1296 Asp Glu Tyr Val Gln Lys Met Thr Phe Asp Ser Tyr Leu Tyr Lys Arg			
420	425	430	
gtt gcg ccg ggt agt cct ttg gag gat atc aag ttg gct gtg aac acc 1344 Val Ala Pro Gly Ser Pro Leu Glu Asp Ile Lys Leu Ala Val Asn Thr			
435	440	445	
att gga agt ttg gtt agg gct aat gct cta agg aga gag att gag aag 1392 Ile Gly Ser Leu Val Arg Ala Asn Ala Leu Arg Arg Glu Ile Glu Lys			
450	455	460	
ctt agt gtt taagaaaacaa ataatgaggt ctatctcctt tcttcatctc 1441 Leu Ser Val			
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<400> 8

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		20					25					30			
Leu	Pro	Gln	Arg	Arg	Thr	Ser	Leu	Arg	Val	Thr	Ala	Ala	Arg	Ala	Thr
	35					40					45				
Pro	Lys	Leu	Ser	Asn	Arg	Lys	Leu	Arg	Val	Ala	Val	Ile	Gly	Gly	Gly
	50				55				60						
Pro	Ala	Gly	Gly	Ala	Ala	Ala	Glu	Thr	Leu	Ala	Gln	Gly	Gly	Ile	Glu
	65					70			75			80			
Thr	Ile	Leu	Ile	Glu	Arg	Lys	Met	Asp	Asn	Cys	Lys	Pro	Cys	Gly	Gly
		85					90				95				
Ala	Ile	Pro	Leu	Cys	Met	Val	Gly	Glu	Phe	Asn	Leu	Pro	Leu	Asp	Ile
		100				105					110				
Ile	Asp	Arg	Arg	Val	Thr	Lys	Met	Lys	Met	Ile	Ser	Pro	Ser	Asn	Ile
	115					120				125					
Ala	Val	Asp	Ile	Gly	Arg	Thr	Leu	Lys	Glu	His	Tyr	Ile	Gly	Met	
	130				135				140						
Val	Arg	Arg	Glu	Val	Leu	Asp	Ala	Tyr	Leu	Arg	Glu	Arg	Ala	Glu	Lys
	145				150				155			160			
Ser	Gly	Ala	Thr	Val	Ile	Asn	Gly	Leu	Phe	Leu	Lys	Met	Asp	His	Pro
		165					170				175				
Glu	Asn	Trp	Asp	Ser	Pro	Tyr	Thr	Leu	His	Tyr	Thr	Glu	Tyr	Asp	Gly
		180				185				190					
Lys	Thr	Gly	Ala	Thr	Gly	Thr	Lys	Lys	Thr	Met	Glu	Val	Asp	Ala	Val
		195				200				205					
Ile	Gly	Ala	Asp	Gly	Ala	Asn	Ser	Arg	Val	Ala	Lys	Ser	Ile	Asp	Ala
		210				215				220					

Gly Asp Tyr Asp Tyr Ala Ile Ala Phe Gln Glu Arg Ile Arg Ile Pro  
225 230 235 240

Asp Glu Lys Met Thr Tyr Tyr Glu Asp Leu Ala Glu Met Tyr Val Gly  
245 250 255

Asp Asp Val Ser Pro Asp Phe Tyr Gly Trp Val Phe Pro Lys Cys Asp  
260 265 270

His Val Ala Val Gly Thr Gly Thr Val Thr His Lys Gly Asp Ile Lys  
275 280 285

Lys Phe Gln Leu Ala Thr Arg Asn Arg Ala Lys Asp Lys Ile Leu Gly  
290 295 300

Gly Lys Ile Ile Arg Val Glu Ala His Pro Ile Pro Glu His Pro Arg  
305 310 315 320

Pro Arg Arg Leu Ser Lys Arg Val Ala Leu Val Gly Asp Ala Ala Gly  
325 330 335

Tyr Val Thr Lys Cys Ser Gly Glu Gly Ile Tyr Phe Ala Ala Lys Ser  
340 345 350

Gly Arg Met Cys Ala Glu Ala Ile Val Glu Gly Ser Gln Asn Gly Lys  
355 360 365

Lys Met Ile Asp Glu Gly Asp Leu Arg Lys Tyr Leu Glu Lys Trp Asp  
370 375 380

Lys Thr Tyr Leu Pro Thr Tyr Arg Val Leu Asp Val Leu Gln Lys Val  
385 390 395 400

Phe Tyr Arg Ser Asn Pro Ala Arg Glu Ala Phe Val Glu Met Cys Asn  
405 410 415

Asp Glu Tyr Val Gln Lys Met Thr Phe Asp Ser Tyr Leu Tyr Lys Arg  
420 425 430

Val Ala Pro Gly Ser Pro Leu Glu Asp Ile Lys Leu Ala Val Asn Thr  
435 440 445

Ile Gly Ser Leu Val Arg Ala Asn Ala Leu Arg Arg Glu Ile Glu Lys  
450 455 460

Leu Ser Val  
465